

# BIOBASE Training Workshop

## Sponsored by the Cushing/Whitney Medical Library\*

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**Date/time:** Friday, August 15, 2014 from 9 AM – 3 PM

**Location:** The Anlyan Center Auditorium (N 107)

**Presenter:** Dr. Alex Kaplun, Field Applications Scientist, BIOBASE

Free and open to all Yale faculty, students, and staff but **registration required.**

**Please register here:** <http://schedule.yale.edu/event.php?id=703746>

Lunch will be provided for registrants.

## Program

### **9:00 AM -12:00PM BIOBASE Knowledge Library (Proteome/TRANSFAC)**

Interested in finding out what's known in the scientific literature about a particular gene, disease or drug? Want to apply that information to high-throughput data analysis? Interested in finding out about transcription factors related to your research? Learn to search the BIOBASE Knowledge Library (BKL) by topic or multi-gene data sets and how to analyze your high throughput data.

PROTEOME™'s powerful ontology search query system, with specialized tools for gene set analysis and pathway visualization, allows scientists to quickly find answers to questions relevant to their research. It works seamlessly with TRANSFAC®, an internationally unique knowledgebase containing data on eukaryotic transcription factors, their experimentally-proven binding sites, and regulated genes, which supports research into gene regulation. Based on TRANSFAC®'s broad compilation of binding sites, positional weight matrices are derived which can be used with the included Match™ tool to search DNA sequences for predicted transcription factor binding sites.

#### *In the PROTEOME™ section, attendees will learn to:*

- search for individual gene, disease, and drug reports by name
- browse for sets of genes, diseases, and drugs which share a desired set of characteristics
- upload a list of genes and identify those characteristics which are statistically over-represented
- export annotated characteristics for a gene list

- visualize protein-protein networks, overlaid with disease and drug assignments
- annotate custom sequences

*In the TRANSFAC section, attendees will learn to:*

- search for individual transcription factors, their experimentally-characterized binding sites and regulated genes, and ChIP experiments
- predict transcription factor binding sites within a promoter or DNA sequence
- create positional weight matrix for transcription factor and compare it to TRANSFAC library of matrices
- search for reported miRNA effects on transcription.

## **12:00 -12:30PM Lunch**

## **12:30 -2:00PM ExPlain**

Interested in microarray, ChIP-chip or ChIP-seq analysis? Biobase's ExPlain™ is a unique upstream data analysis system that combines promoter and pathway analysis tools and enables you to identify transcription factors affecting gene expression in your microarray and RNA-Seq experiments, as well as predict how they, in combination, can induce observed gene expression patterns. Come learn how to take your analysis further and gain insight into the key upstream signaling regulators influencing the activity of these transcription factors.

## **2:15 -3:00PM Human Gene Mutation Database (HGMD)**

Got mutations? HGMD® Professional is a unique resource providing comprehensive data on human inherited disease mutations. Its compilation of structured, manually curated data from the peer-reviewed literature enables quick access to both single mutation queries and advanced search applications. HGMD® is widely used in human genetics research, diagnostics, and personal genomics applications.

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